the hypothesis that the QTN is of Chinese origin. Chinese Meishan and Erhualian are two subgroups of the Taihu breed.[6] Both historical records and molecular data indicate that Chinese domestic pigs were introduced into Europe in the 19th century.[7] Considering our observation of the mutant *A* allele in some Chinese breeds and the Chinese origin of the *Q* chromosome, it is conceivable that the 3072G>A transition occurred in China either during or after domestication and that the favourable *A* allele was introgressed into European domestic pigs about 200 years ago. The frequency of allele *A* increased gradually in Western commercial pig populations because of the intensive selection in growth and carcass traits. Whether the mutation arose before or after pig domestication in China is still unknown; analysis of Chinese wild pigs may resolve this.

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W-specific microsatellite loci detected by *in silico* analysis map to chromosome Z of the chicken genome

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Description: Avian females are the heterogametic gender (ZW) and males are homogametic (ZZ). The non-recombining, female-specific regions on the W chromosome are maternally inherited. As such, they have special value for matrilineal phylogenetic analyses of avian populations. The use of Y-specific microsatellites for phylogenetic analysis was shown to be highly powerful in human populations.[1] W-specific regions may also be important for studies on the evolution of sex chromosomes[2] and for gender identification.[3] It has been suggested that the Z and W chromosomes in the avian genome evolved from a common autosomal ancestor.[4] During evolution, recombination between some regions of the Z and W chromosomes became impossible, probably due to chromosomal inversions.[4] The aim of this study was to detect microsatellite loci in W-specific regions of the chicken genome that do not have homologues on any other chromosome, including the Z chromosome.

Microsatellite identification: We used approximately 5 Mb of the W chromosome sequence from the draft genome assembly (WASHUC1) as input into the Tandem Repeats Finder[5] program. We found 173 microsatellite loci that contained 2- to 6-bp repeat motifs with eight or more repeats. Loci were analysed for W specificity using BLAST.[6] Primers were designed by Primer3 software.[7]

The expectation was that the polymerase chain reaction (PCR) would amplify fragments specific to the W chromosome. Twenty-five microsatellite loci were tested by PCR for gender specificity on at least four males and four females. Unexpectedly, PCR products were generated with DNA from males as well as with DNA from females.

Linkage mapping: Sixteen markers were tested for informativeness in the East Lansing reference panel. Fourteen of the 16 (Table 1) were genotyped for potential linkage to 1200+ previously mapped loci, as described by Liu and Cheng.[8] In all cases, the 'W-specific' microsatellites mapped to chromosome Z, and except for one microsatellite, to approximately the same 6-cM region (Table 1).

Comments: The outcomes of this study include the identification of 14 previously unreported microsatellites on the chicken Z chromosome. Furthermore, the results indicate that the draft chicken assembly of W-specific regions is erroneous. Specifically, as the majority of our mapped microsatellites were located within the five large supercontigs that spanned from 721 718 to 4 842 841 bp of the chromosome W sequence, it is likely that the majority of chromosome W is incorrectly assigned.

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Table 1 Microsatellite loci detected *in silico* in the chicken genome sequence.

Marker	Accession number	Repeat motif	Forward primer (5′ → 3′)	Reverse primer (3′ → 5′)	*In silico* product size (bp)	Position on Z chromosome (cM)[1]
HUR0401	BV680360	$(ATTT)_{12}$	GCAGAAGGCTGCTTTTCACT	TTTCGGTGAATGTTCTGCTG	259	122
HUR0402	BV680361	$(TG)_{13}$	TGGAAATGAACCCAACTCCT	GTGGTCACAGAACAGCTCCA	228	175
HUR0403	BV680362	$(AAT)_{15}$	ATGGCTTAAGCATCATAAAG	TAGGTGCATTCCAACTCAAC	231	175
HUR0404	BV680363	$(AG)_{16}$	AAGAATAAAAGGACAGGTTG	ATTAGGTGCACTGAAAGAAG	159	173
HUR0405	BV680364	$(AAT)_{16}$	GTCTCGTACGACCTGTCCCA	GGTGGTTTCCGAACACCTTA	330	173
HUR0406	BV680365	$(TTA)_{13}$	TATTAGTATTTAGGCTTTGG	TTTGGAGTTCAGTTCATAAC	216	171
HUR0407[2]	–	$(TC)_{10}$	GAAGAAAGAAGCGGCACTTG	AAAAAGCACGCTCGGTATGT	265	–
HUR0408	BV680366	$(TTG)_{9}$	GTCTTTTACCAGCAGAGGCG	CCACAGATGGAACAACCAGA	270	169
HUR0409[2]	–	$(TG)_{15}$	CTCTTTGCTAACCCGAGTTG	GCCCAAATTGTAGATTCAGG	265	–
HUR0410	BV680367	$(AC)_{17}$	GAAGGTATGTAATGTTTTGG	TGCTGTACTTATCCAGATTG	128	169
HUR0411	BV680368	$(AC)_{16}$	CTGTTCTGCATTTTAGTTTG	AATTTGTACTTGTTCCTTCC	157	169
HUR0412	BV680369	$(TA)_{17}$	AGGAGTCATCTTCGGCAAAA	TTTTGGCTAACAGGAGGCTT	191	169
HUR0413	BV680370	$(AAT)_{18}$	GCAGGGCTTGTTTTATGGTT	TGCTCAAACAGCCATTGAAG	246	169
HUR0414	BV680371	$(TA)_{20}$	TACTATAGATGTGATGTATG	ATTGAATTAGGGTTATGTAG	139	169
HUR0415	BV680372	$(TTTC)_{20}$	TAATAGTGCTGTGCCGTAAG	AGAGCTAGTTAGTCCTGGAA	261	169
HUR0416	BV680373	$(AT)_{14}$	CTTGAGTTTCAGAGCCATAC	TGAACTAGCTGCTTCTACAG	146	169

[1]cM, centiMorgan on the East Lansing chicken map (http://poultry.mph.msu.edu).
[2]Non-informative in the East Lansing reference panel.

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Radiation hybrid mapping and sequence analysis of 21 genes on porcine chromosome 15

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Source/description: Porcine genomic DNA was extracted from ear samples of pigs representing four breeds (Duroc, Erhualian, Dahuabai and Landrace). For each breed, a DNA pool was constructed using 30 samples.

Radiation hybrid mapping and chromosomal assignments: Mapping of 21 genes was carried out by typing primers listed in Table S1 across the porcine IMpRH panels[1] using procedures described at http://www.toulouse.inra.fr/lgc/pig/RH/IMpRH.htm (last accessed 22 February 2006).[2] Two-point and multipoint analyses were carried out with assignment of markers on the current IMpRH map (http://www.intl-pag.org/pag/10/abstracts/PAGX_P607.html (last accessed 22 February 2006)) at LOD ≥ 6.0. Chromosomal assignments and the nearest linked markers for the genes are provided in Table 1. An integrated RH map of porcine chromosome 15 (SSC15) and a comparative map of SSC15 and HSA2 are presented in Fig. 1. Our study further supports the existence of conserved synteny between HSA2 and SSC15.[3]

Polymorphism identification: For each of the 21 genes, PCR products that were generated from the four breed DNA pools were sequenced. Sequences were submitted to GenBank and assigned accession numbers from AY805665 to AY805748 (Table 1). Polymorphisms identified in the sequences were given IUB ambiguity codes. In total, 19 polymorphic positions were identified across the 8943 bp of sequence that was analysed.

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Supplementary Material

The following supplementary material is available online at http://www.blackwell-synergy.com:
Table S1 Primer information.